Figure 1A

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dihydrokaempferol

chalcone isomerase

HO

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chalcone synthase

3 x malonyl-CoA

HO. <del>.</del> 2',4,4',6'-tetrahydroxychalcone

flavanone-3-hydroxylase

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p-coumaroyl-CoA

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naringenin

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10 20 30 40 50 60	SETVCVTGASGYIGS	MGSASESVCVTGASGFIGSWLVMRLIERGYTVRATVRDPVNMKKVKHLVELPGAK MDQTLTHTGSKKACVIGGTGNLASILIKHLLQSGYKVNTTVRDPENEKKIAHLRQLQEL-	70 80 90 100 110 120	+ SKLSIWKAELTEEGSFDEAIKGCTGVFHLATPVDFKSKDPENEMIKPTIQGVLNIMKACL SKLSIWKAELTEEGSFDEAIKGCTGVFHLATPVDFKSKDPENEMIKPTIQGVLNIMKACL	SKLSLWKADLAEEGSFDEAIKGCTGVFHVATPMDFESKDPENDMIKPAITGVLNVLKACV SKLSLWKADLAEEGSFDEAIKGCTGVFHVATPMDFESKDPENEVIKPTINGVLDIMKACL GDLKIFKADLTDEDSFESSFSGCEYIFHVATPINFKSEDPEKDMIKPAIQGVINVLKSCL	130 140 150 160 170 180	KAKTVRRLVFTSSAGTTNITEHQKPIIDETCWTDVEFCRRLNMTGWMYFVSKTLAEKE KAKTVRRLVFTSSAGTTNITEHQKPIIDETCWTDVEFCRRLNMTGWMYFVSKTLAEKE	RAKGVKRVILTSSAAAVTINQLKGTDLVMDESNWTDVEYLSTAKPPTWGYPASKALAEKA KAKTVRRIIFTSSAGTLNVIERQKPVFDDTCWSDVEFCRRVKMTGWMYFVSKTLAEKE	KSKSVKKV1YTSSAAAVSINNLSGTGLVMNEENWTDIDELTEEKPFNWGYPISKVLAEKK
	SEQ ID NO:4 SEQ ID NO:6	111		888	SEQ ID NO: 17 SEQ ID NO: 17 SEQ ID NO: 18		CI CI	225	ST:ON OT DES

Figure 2

227 227 156 227 239	286 286 216 286 299	337 337 255 345
+  190 210 220 230 240 AWKFAKEHGMDEIAILPALVIGPELLPTMPSSVISALSPINGIEAHYSIIKQAQ AWKFAKEHGMDEIAILPALVIGPELLPTIPSSVISALSPINGIEAHYSIIKQAQ AWKFAKEHGMDEIAILPALVIGPELLPTIPSSVISALSPINGIEAHYSIIKQAQ AWKFAKEQGLDFITIIPPLVVGPFLMPTMPPSLITALSPITGNDFLINALKGMQLLSGSI AWKFAKEQGLDFITIIPPLVVGPFLMPTMPPSLITALSPITGNEDHYSIIKQQQ AWEFAEENKINLVTVIPALIAGNSLLSDPPSSLSLSMSFITGKEMHVTGLKEMQKLSGSI	++	310 320 340 340 350 360  LEPVRESSKKITDLGFQFKYSLEDMYTGAIDTCIEKGLLPKPAEIPANGIE LEPVRESSKKITDLGFQFKYSLEDMYTGAIDTCIEKGLLPKPAE
SEQ ID NO:4 SEQ ID NO:6 SEQ ID NO:8 SEQ ID NO:17 SEQ ID NO:17	SEQ ID NO:4 SEQ ID NO:6 SEQ ID NO:8 SEQ ID NO:17 SEQ ID NO:18	SEQ ID NO:4 SEQ ID NO:6 SEQ ID NO:8 SEQ ID NO:17 SEQ ID NO:18

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339 339 256 347 342

Figure 2C

SEQ ID NO:4 SEQ ID NO:6 SEQ ID NO:8 SEQ ID NO:17 SEQ ID NO:18

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10 20 30 40 50 60	MANTSKGKVCVTGASGEVGSWLVMKLLQVGYTVRATVRDPANVEKNKPLLELPGAKERLS MANTSKGKVCVTGASGEVASWLVMKLLGSGYHVLGTVRDPGNQKKVAHLWNLAGAKEGLE M-DGSKGPVVVTGASGEVGSWLVMKLLQAGYTVRATVRDPANVEKNKPLLELPGAKERLS M-DGNKGPVVVTGASGEVGSWLVMKLLQAGYTVRATVRDPANVEKTKPLLELPGAKERLS M-DGNKGPVVVTGASGEVGSWLVMKLLQAGYTVRATVRDPANVEKTKPLLELPGAKERLS MVISSKGKVCVTGASGEVASWLIKRLLEAGYHVIGTVRDPSNREKVSHLWRLPSAKERLQ	+++  70 80 90 110 120  120 120 ++  IWKADLSEEGSFDDAIAGCTGVFHVATPMDFDSQDP-ENEVIKPTVEGMLSIMRACKEAG  LVRADLLEEGSFDDAVMACEGVFHTASPIITNADSKEEMLDSAINGTLNVLRSCKKNP  IWKADLSDEGSFDDAIAGCTGVFHVATPMDFDSKDP-ENEVIKPTVEGMLSIMRACKEAG  IWKADLSEGSFNEAIAGCTGVFHVATPMDFDSQDP-ENEVIKPTVEGMLSIMRACKEAG  IWKADLSEGSFNEAIAGCTGVFHYATPMDFDSQDP-ENEVIKPTVEGMLSIMRACKEAG  LVRADLMEEGSFDDAVMACEGVFHTASPVLAKSDSNCKEEMLVPAINGTLNVLKSCKKNP	130 140 150 160 170 180 ++  TVKRIVETSSAGSVNIEERQRPAYDQDNWSDIDFCRRVKMTGWMYEVSKSLAEKAA FLKRVVLTSSAGSVNIEERQRPAYDQDNWSDIDFCRRVKMTGWMYEVSKSLAEKAA TVKRIVETSSAGSVNIEERQRPAYDQDNWSDIDFCRRVKMTGWMYEVSKSLAEKAA TVKRIVETSSAGSVNIEERQRPAYDQDNWSDIDFCRRVKMTGWMYEVSKSLAEKAA TVKRIVFTSSAGSVNIEERPRPAYDQDNWSDIDYCRRVKMTGWMYEVSKALAEKAA FLKRVVLTSSSSTVRIMDESK-HPEISLDETIWSSVALCEKLQLW-YALAKISAEKAA
	SEQ ID NO:12 SEQ ID NO:14 SEQ ID NO:16 SEQ ID NO:20 SEQ ID NO:20	SEQ ID NO:12 SEQ ID NO:14 SEQ ID NO:16 SEQ ID NO:20 SEQ ID NO:20	SEQ ID NO:12 SEQ ID NO:14 SEQ ID NO:16 SEQ ID NO:19 SEQ ID NO:20

+240		300		360	
+ 2	TAHIDDI KVHIDDI KVHIDDI KVHIDDI KVHIDDI	+	+ 2PIHESS 2TYGYNT 2PIHESS 2PIHESS	+350	-+ AAGEGQAIGAET REGAA AAGKGQAIGAET AAGEGQAIGAET
230	ILKQVQ SILKQVQ SILKQVQ SILKQVQ	290	GVDDDLG NIYGE-G GVDDDLG GVDDNLG	350	LAAGEGG
220	.alitgneahys .alitgneahys .alitgneahys .alitgneahys	280	TEPEYSIPQKEA FPSFPIPKSLP FPEYSIPHKFA FPEYDIPQKFA	340	PPPAGGKLGA
210	PPSLVTAI GPTASDVI PPSLVTAI PPSLVTAI SVTASDII	270	-+ LARMLRDR LVALLAKR LARMLRDR LARMLQDR LVALLAKQ	330	+ KGLIPLGDA HGYL KGLIPLGDA KGLIPLGDV
200	VVGPFLSAGM TIGPNLSPVL VVGPFLSAGM VVGPFLSAGM VVGPFLSAGM	260 270 280	CSSHDATIHG CNSAVLDSNE CSSHDATIHG CSSHDATIHG CSSHDATIHG	320	MEDAAIRTCREK MEDASIRTCREK MEDAAIRTCREK MEDAAIHTCRDK MEGDCVESIKDO
190	MEYASENGLDEISIIPTLVVGPFLSAGMPPSLVTALALITGNEAHYSILKQVQLVHLDDL WEFAKENNIDLVAVLPTFIIGPNLSPVLGPTASDVLGLFKGETEKFTIFGRMGYVHIDDV MEYASENGLDFISIIPTLVVGPFLSAGMPPSLVTALALITGNEAHYSILKQVQLVHLDDL MEYASENGLDFISIIPTLVVGPFLSAGMPPSLVTALALITGNEAHYSILKQVQLVHLDDL WEFAKENNIDLVTVLPSFVIGPSLSHELSVTASDILGLLQGDTDRFISYGRMGYVHIDDV	250	CDAMTFLFEHPEANGRYICSSHDATIHGLARMLRDRFPEYSIPQKFAGVDDDLQPIHFSS ASCHILVYETADAKGRYICNSAVLDSNELVALLAKRFPSFPIPKSLPNIYGE-QTYGYNT CDAMTFLFEHPEANGRYICSSHDATIHGLARMLRDRFPEYSIPHKFAGVDDDLQPIHFSS CDAMTFLFEHPEANGRYICSSHDATIHGLARMLQDRFPEYDIPQKFAGVDDNLQPIHFSS ASCHILVYEAPQATGRYLCNSVVLDNNELVALLAKQFPIFPIPRSLRNPYEK-QSYELNT	310	KKLLDHGESERYTAEDMFDAAIRTCREKGLIPLGDAPPPAAGGKLGALAAGEGQAIGAETSKLLDHGESERYTAEDMFDAAIRTCREKGLIPLGDAPPPAAGGKLGALAAGEGQAIGAETSKIRKLGLEFR-GVEEMFDDSVESLKAHGYL
	MEYASI WEFAKI MEYASI MEYASI WEFAKI		CDAMTI ASCHII CDAMTI CDAMTI		KKLLDH SKIRKI KKLLDH KKLLDH SKIQQI
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